

C. STROUP

1633

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/391,861

DATE: 10/30/2000
TIME: 14:29:32

Input Set: I391861.RAW

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This Raw Listing contains the General Information
Section and up to first 5 pages.

NOV 13 2000

TECH CENTER 1600/2900

ENTERED
see p. 5

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1 <110> APPLICANT: Thomason, Arlen
2   Liu, Benxian
3 <120> TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
4 <130> FILE REFERENCE: 99,371
5 <140> CURRENT APPLICATION NUMBER: US/09/391,861
6 <141> CURRENT FILING DATE: 1999-09-07
7 <160> NUMBER OF SEQ ID NOS: 41
8 <170> SOFTWARE: PatentIn Ver. 2.0
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11 <212> TYPE: DNA
12 <213> ORGANISM: Homo sapiens
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19   acctgaggac ccgagccatt g atg gac tcg gac gag acc ggg ttc gag cac 171
20                               Met Asp Ser Asp Glu Thr Gly Phe Glu His
21                               1           5           10
22   tca gga ctg tgg gtt tct gtg ctg gct ggt ctt ctg ctg gga gcc tgc 219
23   Ser Gly Leu Trp Val Ser Val Leu Ala Gly Leu Leu Leu Gly Ala Cys
24                               15           20           25
25   cag gca cac ccc atc cct gac tcc agt cct ctc ctg caa ttc ggg ggc 267
26   Gln Ala His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly
27                               30           35           40
28   caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa 315
29   Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu
30                               45           50           55
31   gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac 363
32   Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp
33                               60           65           70
34   cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt 411
35   Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val
36   75           80           85           90
37   att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca 459
38   Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro
39                               95           100          105
40   gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc 507
41   Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser
42                               110          115          120
43   ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa 555
44   Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu
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 46 gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg 603
 47 Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg
 48 140 145 150
 49 gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg 651
 50 Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu
 51 155 160 165 170
 52 ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc 699
 53 Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro
 54 175 180 185
 55 gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc 747
 56 Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly
 57 190 195 200
 58 cga agc ccc agc tac gct tcc tga' agccagaggc tgtttactat gacatctcct 801
 59 Arg Ser Pro Ser Tyr Ala Ser
 60 205 210
 61 ctttatttat taggttatatt atcttatatta tttttttatt tttcttactt gagataataa 861
 62 agagttccag aggaggataa gaatgagcat gtgtgagtgt ctgagggaag acatggcagc 921
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 64 tcctggcttc ccaactgggcc tcaactttttt cttttctttt cttttctttt ttttgagacg 1041
 65 gagtcctcgt ctgcactcca gcccaggcca cagagcgaga ttccatctca aaaaaataaa 1101
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 75 Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
 76 20 25 30
 77 Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
 78 35 40 45
 79 Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
 80 50 55 60
 81 Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
 82 65 70 75 80
 83 Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
 84 85 90 95
 85 Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
 86 100 105 110
 87 Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
 88 115 120 125
 89 Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
 90 130 135 140
 91 His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
 92 145 150 155 160
 93 Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
 94 165 170 175

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101     <211> LENGTH: 649
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103     <213> ORGANISM: Mus musculus
104     <220> FEATURE:
105     <221> NAME/KEY: CDS
106     <222> LOCATION: (1)..(630)
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110             1                      5                      10                      15
111     ctg ctg ctg gct gtc ttc ctg ctg ggg gtc tac caa gca tac ccc atc      96
112     Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln Ala Tyr Pro Ile
113             20                      25                      30
114     cct gac tcc agc ccc ctc ctc cag ttt ggg ggt caa gtc cgg cag agg      144
115     Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg
116             35                      40                      45
117     tac ctc tac aca gat gac gac caa gac act gaa gcc cac ctg gag atc      192
118     Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile
119             50                      55                      60
120     agg gag gat gga aca gtg gta ggc gca gca cac cgc agt cca gaa agt      240
121     Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser
122             65                      70                      75                      80
123     ctc ctg gag ctc aaa gcc ttg aag cca ggg gtc att caa atc ctg ggt      288
124     Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly
125             85                      90                      95
126     gtc aaa gcc tct agg ttt ctt tgc caa cag cca gat gga gct ctc tat      336
127     Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr
128             100                     105                     110
129     gga tcg cct cac ttt gat cct gag gcc tgc agc ttc aga gaa ctg ctg      384
130     Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu
131             115                     120                     125
132     ctg gag gac ggt tac aat gtg tac cag tct gaa gcc cat ggc ctg ccc      432
133     Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro
134             130                     135                     140
135     ctg cgt ctg cct cag aag gac tcc cca aac cag gat gca aca tcc tgg      480
136     Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp
137     145                     150                     155                     160
138     gga cct gtg cgc ttc ctg ccc atg cca ggc ctg ctc cac gag ccc caa      528
139     Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln
140             165                     170                     175
141     gac caa gca gga ttc ctg ccc cca gag ccc cca gat gtg ggc tcc tct      576
142     Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser
143             180                     185                     190
144     gac ccc ctg agc atg gta gag cct tta cag ggc cga agc ccc agc tat      624

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 147 gcg tcc tgactctttc ctgaatcta 649
 148 Ala Ser
 149 210

150 <210> SEQ ID NO 4
 151 <211> LENGTH: 210
 152 <212> TYPE: PRT
 153 <213> ORGANISM: Mus musculus
 154 <400> SEQUENCE: 4
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 157 Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln Ala Tyr Pro Ile
 158 20 25 30
 159 Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg
 160 35 40 45
 161 Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile
 162 50 55 60
 163 Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser
 164 65 70 75 80
 165 Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly
 166 85 90 95
 167 Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr
 168 100 105 110
 169 Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu
 170 115 120 125
 171 Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro
 172 130 135 140
 173 Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp
 174 145 150 155 160
 175 Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln
 176 165 170 175
 177 Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser
 178 180 185 190
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 180 195 200 205
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183 <210> SEQ ID NO 5
 184 <211> LENGTH: 181
 185 <212> TYPE: PRT
 186 <213> ORGANISM: Homo sapiens
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 190 Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
 191 20 25 30
 192 Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser
 193 35 40 45
 194 Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln

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196  Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly
197      65      70      75      80
198  Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg
199      85      90      95
200  Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
201      100     105     110
202  Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro
203      115     120     125
204  Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro
205      130     135     140
206  Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val
207      145     150     155     160
208  Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser
209      165     170     175
210  Pro Ser Tyr Ala Ser
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213  <211> LENGTH: 181
214  <212> TYPE: PRT
215  <213> ORGANISM: Mus musculus
216  <400> SEQUENCE: 6
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219  Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Gln Asp Thr Glu Ala His
220      20      25      30
221  Leu Glu Ile Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser
222      35      40      45
223  Pro Glu Ser Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln
224      50      55      60
225  Ile Leu Gly Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly
226      65      70      75      80
227  Ala Leu Tyr Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg
228      85      90      95
229  Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
230      100     105     110
231  Gly Leu Pro Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala
232      115     120     125
233  Thr Ser Trp Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His
234      130     135     140
235  Glu Pro Gln Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val
236      145     150     155     160
237  Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser
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241  <210> SEQ ID NO 7
242  <211> LENGTH: 21
243  <212> TYPE: DNA
244  <213> ORGANISM: Mus musculus

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I391861.RAW

Line ? Error/Warning

Original Text

60 W Invalid/Missing Amino Acid Numbering
939 W "N" or "Xaa" used: Feature required

205 210
ggaaggaaaa aagcggccgc aacannnnnn nnn